



SEQUENCE LISTING

<110> John, Varghese
Sinha, Sukanto
Tung, Jay

<120> BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS

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<141> 2000-12-02

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<170> PatentIn version 3.3

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Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
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Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
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Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
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<210> 49
<211> 32
<212> DNA

<213> Homo sapiens

<400> 49

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32

<210> 50

<211> 11

<212> PRT

<213> Homo sapiens

<400> 50

Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val

1 5 10

<210> 51

<211> 5

<212> PRT

<213> Homo sapiens

<400> 51

Val Asn Leu Asp Ala

1 5

<210> 52

<211> 9

<212> PRT

<213> Artificial

<220>

<223> Synthetic oligopeptide substrate

<400> 52

Ser Glu Val Asn Leu Asp Ala Glu Phe

1 5

<210> 53

<211> 30

<212> PRT

<213> Artificial

<220>

<223> Synthetic oligopeptide substrate

<400> 53

Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile

1 5 10 15

Lys Thr Glu Glu Ile Ser Glu Val Asn Leu Asp Ala Glu Phe

20 25 30

<210> 54

<211> 5
<212> PRT
<213> Homo sapiens

<400> 54

Val Lys Met Asp Ala
1 5

<210> 55
<211> 24
<212> PRT
<213> Homo sapiens

<400> 55

Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
1 5 10 15

Glu Met Val Asp Asn Leu Arg Gly
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<210> 56
<211> 15
<212> PRT
<213> Homo sapiens

<400> 56

Ile Ser Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg
1 5 10 15

<210> 57
<211> 419
<212> PRT
<213> Homo sapiens

<400> 57

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
 180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
 195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
 210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
 225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
 245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
 260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
 275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
 290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
 305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
 325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
 340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
 355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
 370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
 385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
 405 410 415

Val Ser Ala

<210> 58
 <211> 407
 <212> PRT
 <213> Homo sapiens

<400> 58

Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
 1 5 10 15

Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val
 20 25 30

Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp
 35 40 45

Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu
 50 55 60

His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg
 65 70 75 80

Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu
 85 90 95

Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg

100						105						110					
Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly		
		115					120					125					
Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg		
	130					135					140						
Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr		
145					150					155					160		
His	Val	Pro	Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro		
				165					170					175			
Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile		
			180					185					190				
Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro		
		195					200					205					
Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile		
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Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys		
225					230					235					240		
Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val		
				245					250					255			
Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys		
			260					265					270				
Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala		
		275					280					285					
Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met		
	290					295					300						
Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln		
305					310					315					320		
Tyr	Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr		
				325					330					335			
Lys	Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val		
			340					345					350				

Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile
 355 360 365

Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala
 370 375 380

Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr
 385 390 395 400

Asn Ile Pro Gln Thr Asp Glu
 405

<210> 59
 <211> 452
 <212> PRT
 <213> Homo sapiens

<400> 59

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
 1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
 20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
 180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
 195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
 210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
 225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
 245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
 260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
 275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
 290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
 305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
 325 330 335

Pro' Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
 340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
 355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
 370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
 180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
 195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
 210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
 225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
 245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
 260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
 275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
 290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
 305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
 325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
 340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
 355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
 370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
 385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
 405 410 415

Val Ser Ala Cys
 420

<210> 61
 <211> 6
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic peptide inhibitor

<220>
 <221> MISC_FEATURE
 <222> (2)..(3)
 <223> Met and Ala are linked by hydroxyethylene molecule

<400> 61

Glu Val Met Ala Glu Phe
 1 5

<210> 62
 <211> 26
 <212> PRT
 <213> Homo sapiens

<400> 62

Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met
 1 5 10 15

Leu Pro Leu Cys Leu Met Val Cys Gln Trp
 20 25

<210> 63
 <211> 33
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(33)
 <223> P26-P4'sw peptide substrate

<400> 63

Cys Gly Gly Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu

1 5 10 15

Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Asn Leu Asp Ala Glu
 20 25 30

Phe

<210> 64
 <211> 29
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <222> (1)..(29)
 <223> P26-P1' peptide substrate with CGG linker

<400> 64

Cys Gly Gly Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu
 1 5 10 15

Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Asn Leu
 20 25

<210> 65
 <211> 501
 <212> PRT
 <213> Homo sapiens

<400> 65

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
 1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
 20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
435 440 445

Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
450 455 460

Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
465 470 475 480

Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp
485 490 495

Ile Ser Leu Leu Lys
500

<210> 66

<211> 480

<212> PRT

<213> Homo sapiens

<400> 66

Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala
1 5 10 15

Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu
20 25 30

Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly

35					40					45					
Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	Met	Thr	Val	Gly	Ser	Pro	Pro
50						55					60				
Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val
65					70					75					80
Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	Arg	Tyr	Tyr	Gln	Arg	Gln	Leu
				85					90					95	
Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val	Tyr	Val	Pro	Tyr	Thr
			100					105					110		
Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp	Leu	Val	Ser	Ile	Pro
		115					120					125			
His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu
	130					135					140				
Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly
145					150					155					160
Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe
				165					170					175	
Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro	Asn	Leu	Phe	Ser	Leu
			180					185					190		
Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala
		195					200					205			
Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr
	210					215					220				
Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu
225					230					235					240
Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp
				245					250					255	
Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr
			260					265					270		
Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile
		275					280					285			

Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly
 290 295 300

Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe
 305 310 315 320

Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe
 325 330 335

Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val
 340 345 350

Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser
 355 360 365

Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val
 370 375 380

Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His
 385 390 395 400

Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr
 405 410 415

Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
 420 425 430

Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe
 435 440 445

Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg Cys
 450 455 460

Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser Leu Leu Lys
 465 470 475 480

<210> 67
 <211> 444
 <212> PRT
 <213> Homo sapiens

<400> 67

Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln
 1 5 10 15

Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn
 20 25 30

Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro
 35 40 45

His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr
 50 55 60

Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp
 65 70 75 80

Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn
 85 90 95

Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe
 100 105 110

Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala
 115 120 125

Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu
 130 135 140

Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly
 145 150 155 160

Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
 165 170 175

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
 180 185 190

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
 195 200 205

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
 210 215 220

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
 225 230 235 240

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
 245 250 255

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val

260	265	270
Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser		
275	280	285
Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile		
290	295	300
Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln		
305	310	315
Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val		
	325	330
		335
Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala		
	340	345
		350
Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu		
	355	360
		365
Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu		
	370	375
		380
Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr		
385	390	395
		400
Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu		
	405	410
		415
Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln		
	420	425
		430
His Asp Asp Phe Ala Asp Asp Ile Ser Leu Leu Lys		
	435	440
<210>	68	
<211>	395	
<212>	PRT	
<213>	Homo sapiens	
<400>	68	
Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln		
1	5	10
		15
Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn		
	20	25
		30

Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro
 35 40 45
 His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr
 50 55 60
 Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp
 65 70 75 80
 Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn
 85 90 95
 Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe
 100 105 110
 Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala
 115 120 125
 Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu
 130 135 140
 Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly
 145 150 155 160
 Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
 165 170 175
 Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
 180 185 190
 Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
 195 200 205
 Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
 210 215 220
 Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
 225 230 235 240
 Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
 245 250 255
 Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
 260 265 270

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
 275 280 285

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
 290 295 300

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
 305 310 315 320

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
 325 330 335

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
 340 345 350

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
 355 360 365

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
 370 375 380

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu
 385 390 395

<210> 69
 <211> 439
 <212> PRT
 <213> Homo sapiens

<400> 69

Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu
 1 5 10 15

Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr
 20 25 30

Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His
 35 40 45

Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys
 50 55 60

Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly
 65 70 75 80

Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala
 85 90 95

Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser
 100 105 110

Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro
 115 120 125

Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His
 130 135 140

Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu
 145 150 155 160

Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly
 165 170 175

Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile
 180 185 190

Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn
 195 200 205

Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser
 210 215 220

Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe
 225 230 235 240

Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe
 245 250 255

Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly
 260 265 270

Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly
 275 280 285

Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr
 290 295 300

Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys
 305 310 315 320

Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile
 325 330 335

Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly
 340 345 350

Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala
 355 360 365

Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn
 370 375 380

Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met
 385 390 395 400

Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys
 405 410 415

Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala
 420 425 430

Asp Asp Ile Ser Leu Leu Lys
 435

<210> 70
 <211> 390
 <212> PRT
 <213> Homo sapiens

<400> 70

Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu
 1 5 10 15

Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr
 20 25 30

Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His
 35 40 45

Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys
 50 55 60

Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly
 65 70 75 80

Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala
 85 90 95

Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser

100					105					110					
Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro
		115					120					125			
Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His
	130					135					140				
Val	Pro	Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu
145				150					155					160	
Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly
				165					170					175	
Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile
			180					185					190		
Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn
		195					200					205			
Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser
	210					215					220				
Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe
225				230						235				240	
Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe
				245					250					255	
Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly
			260					265					270		
Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly
		275					280					285			
Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr
	290					295					300				
Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys
305				310						315				320	
Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile
				325					330					335	
Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly
			340					345					350		

Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala
 355 360 365

Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn
 370 375 380

Ile Pro Gln Thr Asp Glu
 385 390

<210> 71
 <211> 374
 <212> PRT
 <213> Homo sapiens

<400> 71

Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
 1 5 10 15

Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val
 20 25 30

Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp
 35 40 45

Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu
 50 55 60

His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg
 65 70 75 80

Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu
 85 90 95

Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg
 100 105 110

Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly
 115 120 125

Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg
 130 135 140

Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr
 145 150 155 160

His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro
165 170 175

Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile
180 185 190

Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro
195 200 205

Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile
210 215 220

Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys
225 230 235 240

Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val
245 250 255

Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys
260 265 270

Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala
275 280 285

Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met
290 295 300

Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln
305 310 315 320

Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr
325 330 335

Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val
340 345 350

Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile
355 360 365

Gly Phe Ala Val Ser Ala
370

<210> 72
<211> 13
<212> PRT
<213> Artificial

<220>
<223> P10-P4' staD-V peptide inhibitor

<220>
<221> MISC_FEATURE
<222> (9)..(10)
<223> Asn and Val are linked via statine moiety molecule

<400> 72

Lys Thr Glu Glu Ile Ser Glu Val Asn Val Ala Glu Phe
1 5 10

<210> 73
<211> 8
<212> PRT
<213> Artificial

<220>
<223> P4-P4' staD-V peptide inhibitor

<220>
<221> MOD_RES
<222> (4)..(5)
<223> Asn and Val are linked via statine molecule

<400> 73

Ser Glu Val Asn Val Ala Glu Phe
1 5

<210> 74
<211> 431
<212> PRT
<213> Homo sapiens

<400> 74

Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala
1 5 10 15

Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu
20 25 30

Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly
35 40 45

Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro
50 55 60

Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val
65 70 75 80

Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu
 85 90 95

Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr
 100 105 110

Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro
 115 120 125

His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu
 130 135 140

Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly
 145 150 155 160

Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe
 165 170 175

Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu
 180 185 190

Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala
 195 200 205

Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr
 210 215 220

Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu
 225 230 235 240

Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp
 245 250 255

Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr
 260 265 270

Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile
 275 280 285

Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly
 290 295 300

Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe
 305 310 315 320

Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe
325 330 335

Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val
340 345 350

Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser
355 360 365

Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val
370 375 380

Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His
385 390 395 400

Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr
405 410 415

Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu
420 425 430

<210> 75

<211> 361

<212> PRT

<213> Homo sapiens

<400> 75

Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu
1 5 10 15

Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr
20 25 30

Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His
35 40 45

Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys
50 55 60

Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly
65 70 75 80

Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala
85 90 95

Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser
100 105 110

Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro
 115 120 125

Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His
 130 135 140

Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu
 145 150 155 160

Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly
 165 170 175

Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile
 180 185 190

Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn
 195 200 205

Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser
 210 215 220

Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe
 225 230 235 240

Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe
 245 250 255

Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly
 260 265 270

Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly
 275 280 285

Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr
 290 295 300

Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys
 305 310 315 320

Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile
 325 330 335

Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly
 340 345 350

Phe Ala Val Ser Ala Cys His Val His
355 360

<210> 76
<211> 63
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(63)
<223> N = A, C, G, or T

<400> 76
garacngayg argarccnga rgarccnggn mgnmgnggnw snttygtnga ratggtn gay 60
aay 63

<210> 77
<211> 21
<212> PRT
<213> Homo sapiens

<400> 77

Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
1 5 10 15

Glu Met Val Asp Asn
20

<210> 78
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Peptide inhibitor P3-p4' XD-V

<220>
<221> misc_feature
<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<400> 78

Val Met Xaa Val Ala Glu Phe
1 5

<210> 79
<211> 11
<212> PRT
<213> Homo sapiens

<400> 79

Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
1 5 10

<210> 80

<211> 419

<212> DNA

<213> Artificial

<220>

<223> Nucleotide insert in pCF vector

<400> 80

ctgttgggct cgcggttgag gacaaactct tcgcggtctt tccagtactc ttggatcgga 60
aaccgcgcgg cctccgaacg gtactccgcc accgagggac ctgagcgagt ccgcatcgac 120
cggatcggaa aacctctcga ctgttgggggt gagtactccc tctcaaaagc gggcatgact 180
tctgcgctaa gattgtcagt ttccaaaaac gaggaggatt tgatattcac ctggcccgcg 240
gtgatgcctt tgagggtggc cgcgctccatc tggtcagaaa agacaatctt tttgttgtca 300
agcttgaggt gtggcaggct tgagatctgg ccatacactt gagtgacaat gacatccact 360
ttgcctttct ctccacaggt gtccactccc aggtccaact gcaggtcgac tctagaccc 419

<210> 81

<211> 408

<212> PRT

<213> Artificial

<220>

<223> pBS/MuImpain E17 #11 construct

<400> 81

Ser Ile Ser Leu Ile Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met
1 5 10 15

Val Asn Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met
20 25 30

Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly
35 40 45

Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg
50 55 60

Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly
65 70 75 80

Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr
 85 90 95

Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn
 100 105 110

Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn
 115 120 125

Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp
 130 135 140

Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Ile
 145 150 155 160

Pro Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn
 165 170 175

Gln Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly
 180 185 190

Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg
 195 200 205

Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly
 210 215 220

Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile
 225 230 235 240

Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu
 245 250 255

Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro
 260 265 270

Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr
 275 280 285

Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu
 290 295 300

Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu
 305 310 315 320

Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe

Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu
 115 120 125

Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser
 130 135 140

Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Ile Pro Asn
 145 150 155 160

Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Thr
 165 170 175

Glu Ala Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp
 180 185 190

His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu
 195 200 205

Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp
 210 215 220

Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp
 225 230 235 240

Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala
 245 250 255

Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly
 260 265 270

Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro
 275 280 285

Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr
 290 295 300

Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro
 305 310 315 320

Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Val
 325 330 335

Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly
 340 345 350

Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val

355 360 365
 Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly
 370 375 380

 Pro Phe Val Thr Ala Asp Met Glu Asp Cys Gly Tyr Asn Asn Arg Ile
 385 390 395 400

 Gln

 <210> 83
 <211> 231
 <212> PRT
 <213> Artificial

 <220>
 <223> pBS/MuImPain E17 Brain #17 construct

 <400> 83

 Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr
 1 5 10 15

 Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu
 20 25 30

 Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro
 35 40 45

 Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp
 50 55 60

 Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly
 65 70 75 80

 Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr
 85 90 95

 Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Val
 100 105 110

 Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile
 115 120 125

 Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys
 130 135 140

Gln Thr His Ile Pro Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly
 145 150 155 160

Phe Pro Leu Asn Gln Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met
 165 170 175

Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr
 180 185 190

Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val
 195 200 205

Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr
 210 215 220

Asp Lys Ser Ile Val Asp Ser
 225 230

<210> 84
 <211> 380
 <212> PRT
 <213> Artificial

<220>
 <223> pBS/ MuImpain E17 Brain #15 construct
 <400> 84

Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr
 1 5 10 15

Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu
 20 25 30

Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro
 35 40 45

Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp
 50 55 60

Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly
 65 70 75 80

Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr
 85 90 95

Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile
 100 105 110

Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile
 115 120 125

Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys
 130 135 140

Gln Thr His Ile Pro Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly
 145 150 155 160

Phe Pro Leu Asn Gln Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met
 165 170 175

Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr
 180 185 190

Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val
 195 200 205

Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr
 210 215 220

Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys
 225 230 235 240

Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr
 245 250 255

Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp
 260 265 270

Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr
 275 280 285

Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro
 290 295 300

Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp
 305 310 315 320

Cys Tyr Lys Phe Ala Val Ser Gln Ser Ser Thr Gly Thr Val Met Gly
 325 330 335

Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys
 340 345 350

Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg
 355 360 365

Thr Ala Ala Val Glu Gly Pro Phe Val Thr Ala Asp
 370 375 380

<210> 85
 <211> 427
 <212> PRT
 <213> Artificial

<220>
 <223> pBS/MuImpain H#3 construct

<400> 85

Ile Asp Lys Leu Asp Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met
 1 5 10 15

Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met
 20 25 30

Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly
 35 40 45

Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg
 50 55 60

Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly
 65 70 75 80

Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr
 85 90 95

Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn
 100 105 110

Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn
 115 120 125

Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp
 130 135 140

Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Ile
 145 150 155 160

Pro Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn
 165 170 175

Gln Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly
 180 185 190

Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg
 195 200 205

Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly
 210 215 220

Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile
 225 230 235 240

Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu
 245 250 255

Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro
 260 265 270

Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr
 275 280 285

Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu
 290 295 300

Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu
 305 310 315 320

Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe
 325 330 335

Ala Val Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met
 340 345 350

Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe
 355 360 365

Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val
 370 375 380

Glu Gly Pro Phe Val Thr Ala Asp Met Glu Asp Gly Tyr Asn Asn Arg
 385 390 395 400

Ile Pro Ala Ala Arg Gly Ile His Phe Ser Gly Arg His Arg Gly Gly
 405 410 415

Ala Pro Ile Arg Pro Ile Val Ser Arg Ile Asn
420 425

<210> 86
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Wild type APP substrate fragment

<400> 86

Val Lys Met Asp
1

<210> 87
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Swedish APP substrate fragment

<400> 87

Val Asn Leu Asp
1

<210> 88
<211> 11
<212> PRT
<213> Artificial

<220>
<223> Human brain N terminus sequence

<400> 88

Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg
1 5 10

<210> 89
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Recombinant 293T N terminus sequence

<400> 89

Thr Gln His Gly Ile Arg Leu Pro Leu Arg
1 5 10

<210> 90

<211> 9
 <212> PRT
 <213> Artificial

 <220>
 <223> Recombinant 293T N terminus sequence

 <400> 90

 Met Val Asp Asn Leu Arg Gly Lys Ser
 1 5

 <210> 91
 <211> 10
 <212> PRT
 <213> Artificial

 <220>
 <223> Recombinant CosA2 N terminus sequence

 <400> 91

 Gly Ser Phe Val Glu Met Val Asp Asn Leu
 1 5 10

 <210> 92
 <211> 10
 <212> PRT
 <213> Artificial

 <220>
 <223> 10 peptide sequence with Swedish mutation of APP

 <400> 92

 Ser Glu Val Asn Leu Asp Ala Glu Phe Arg
 1 5 10

 <210> 93
 <211> 6
 <212> PRT
 <213> Artificial

 <220>
 <223> Protein composition containing a beta-secretase inhibitor molecule

 <220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> Valine has attached hydrogen, acetyl, t-butoxycarbonyl or carbobenzoyl molecule

 <220>
 <221> MISC_FEATURE
 <222> (2)..(2)
 <223> X = methionine, phenylglycine, n-leucine, asparagine,

phenylalanine, glycine or valine

<220>

<221> MISC_FEATURE

<222> (2)..(3)

<223> Second and third amino acid residues are linked via statine, aha(cyclohexylmethylstatine) or phenylstatine (Phe-sta) wherein the phenyl group may optionally have mono or di-substitution chosen from the group consisting of Cl, F, Br, methyl or methoxy.

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> X = valine, alpha-aminobutyric acid, phenylglycine, or alanine

<400> 93

Val Xaa Xaa Ala Glu Phe
1 5

<210> 94

<211> 6

<212> PRT

<213> Artificial

<220>

<223> Protein composition containing a beta-secretase inhibitor molecule

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Valine has attached hydrogen, acetyl, t-butoxycarbonyl or carbobenzoyl molecule

<220>

<221> MISC_FEATURE

<222> (2)..(3)

<223> Met and Val are connected via statine, aha(cyclohexylmethylstatine) or phenylstatine

<400> 94

Val Met Val Ala Glu Phe
1 5

<210> 95

<211> 6

<212> PRT

<213> Artificial

<220>

<223> Protein composition containing a beta-secretase inhibitor molecule

<220>

<221> MISC_FEATURE
 <222> (1)..(1)
 <223> Valine is acetylated

 <220>
 <221> MISC_FEATURE
 <222> (2)..(2)
 <223> X is phenylglycine

 <220>
 <221> MISC_FEATURE
 <222> (2)..(3)
 <223> Second and third amino acid residues are linked via statine molecule

 <400> 95

Val Xaa Val Ala Glu Phe
 1 5

<210> 96
 <211> 6
 <212> PRT
 <213> Artificial

<220>
 <223> Protein composition containing a beta-secretase inhibitor molecule

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> Valine has attached hydrogen, acetyl, t-butoxycarbonyl or carbobenzoyl molecule

<220>
 <221> MISC_FEATURE
 <222> (2)..(3)
 <223> Leu and Vali are linked via statine molecule

<400> 96

Val Leu Val Ala Glu Phe
 1 5

<210> 97
 <211> 6
 <212> PRT
 <213> Artificial

<220>
 <223> Protein composition containing a beta-secretase inhibitor molecule

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)

<223> Val has attached hydrogen, acetyl, t-butoxycarbonyl or carbobenzoyl molecule

<220>

<221> MISC_FEATURE

<222> (2)..(3)

<223> Asn and Val are linked via statine molecule

<400> 97

Val Asn Val Ala Glu Phe

1

5

<210> 98

<211> 6

<212> PRT

<213> Artificial

<220>

<223> Protein composition containing a beta-secretase inhibitor molecule

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Val has attached hydrogen, acetyl, t-butoxycarbonyl or carbobenzoyl molecule

<220>

<221> MISC_FEATURE

<222> (2)..(3)

<223> Phe and Val are linked via statine molecule

<400> 98

Val Phe Val Ala Glu Phe

1

5

<210> 99

<211> 5

<212> PRT

<213> Artificial

<220>

<223> Protein composition containing a beta-secretase inhibitor molecule

<220>

<221> MISC_FEATURE

<222> (1)..(2)

<223> Met and Val are linked via phenylstatine molecule

<400> 99

Met Val Ala Glu Phe

1

5

<210> 100
<211> 6
<212> PRT
<213> Artificial

<220>
<223> Protein composition containing a beta-secretase inhibitor molecule

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Val is acetylated is Acetyl group

<220>
<221> MISC_FEATURE
<222> (2)..(3)
<223> Met and Val are linked via statine molecule

<400> 100

Val Met Val Ala Glu Phe
1 5

<210> 101
<211> 22
<212> DNA
<213> Homo sapiens

<400> 101
cggccggagg ggcagctttg tg

22